SEQUENCE LISTING

<110> Nakamura, Yusuke
Furukawa, Yoichi
Oncotherapy Science, Inc.

<120> Method for Diagnosing Colorectal Cancers

<130> 082368-008900US

<140> US 10/589,594
<141> 2006-08-15

<150> WO PCT/JP04/02145
<151> 2004-02-24

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2624
<212> DNA
<213> Homo sapiens

<220>
<223> C10orf3

<220>
<221> CDS
<222> (294)...(1688)
<223> C10orf3

<400> 1
ggcacgaggg gccgacgcga gcgccgcgct tcgcttcagc tgctagctgg cccaagggag 60
gcgaccgcgg agggtggcga ggggcggcca ggacccgcag ccccggggcc gggccggtcc 120
ggaccgccag ggagggcagg tcagtgggca gatcgcgtcc gcgggattca atctctgccc 180
gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcacccg gctgggcgcc 240
tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
Met
1

tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
5 10 15

cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
20 25 30

att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
35 40 45

aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc 488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
50 55 60 65

```
ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac   536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
                70                  75                  80

aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act   584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
            85                  90                  95

acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg   632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg
        100                 105                 110

agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa   680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
    115                 120                 125

caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa   728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys
130                 135                 140                 145

acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac   776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
                150                 155                 160

tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct   824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
            165                 170                 175

ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc   872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
        180                 185                 190

tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg   920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
    195                 200                 205

gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca   968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
210                 215                 220                 225

gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg  1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
                230                 235                 240

gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag  1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
            245                 250                 255

ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa  1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln
        260                 265                 270

aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca  1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
    275                 280                 285

gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa  1208
Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
290                 295                 300                 305
```

```
aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag   1256
Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
                310                 315                 320

aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca   1304
Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
            325                 330                 335

tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa   1352
Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
        340                 345                 350

caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac   1400
Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp
    355                 360                 365

cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga   1448
Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
370                 375                 380                 385

aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat   1496
Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
                390                 395                 400

gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa   1544
Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
            405                 410                 415

aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc   1592
Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
        420                 425                 430

aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc   1640
Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
    435                 440                 445

act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag   1688
Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
450                 455                 460

caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg 1748
ggcattttga attatatatt tcacattttg cataaaactg cctatctacc tttgacactc 1808
cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac 1868
ctccctgaca tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg 1928
agactactaa cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt 1988
gctaatgggt taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca 2048
aagataatta accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac 2108
ctacaatcct aattttgatg tccattgtta agaggtggtg atagatacta ttttttttt 2168
catattgtat agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac 2228
cattgaaact taacccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt 2288
ttgaggcata atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac 2348
tgtaacttga attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat 2408
aaacccatgt agccctctca tttgattgac agtattttag ttatttttgg cattcttaaa 2468
gctgggcaat gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt 2528
ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac 2588
tgtaaatgag aaaagaataa aattatttaa tgtttt                          2624
```

<210> 2
<211> 464
<212> PRT
<213> Homo sapiens

<220>
<223> C10orf3

<400> 2

```
Met Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser
 1               5                  10                  15
Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
            20                  25                  30
Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
        35                  40                  45
Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
    50                  55                  60
Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65                  70                  75                  80
Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85                  90                  95
Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
            100                 105                 110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
        115                 120                 125
Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
    130                 135                 140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145                 150                 155                 160
Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
                165                 170                 175
Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
            180                 185                 190
Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
        195                 200                 205
Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
    210                 215                 220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225                 230                 235                 240
Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
                245                 250                 255
Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
            260                 265                 270
Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
        275                 280                 285
Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
    290                 295                 300
Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305                 310                 315                 320
Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
                325                 330                 335
Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
            340                 345                 350
Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
        355                 360                 365
Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
    370                 375                 380
Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385                 390                 395                 400
His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
                405                 410                 415
Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
            420                 425                 430
Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
        435                 440                 445
```

Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
450 455 460

<210> 3
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> GAPDH RT-PCR amplification forward primer

<400> 3
acaacagcct caagatcatc ag 22

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GAPDH RT-PCR amplification reverse primer

<400> 4
ggtccaccac tgacacgttg 20

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 RT-PCR amplification forward primer

<400> 5
agagatccga agagctctta tct 23

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 RT-PCR amplification reverse primer

<400> 6
gatgctcagt ggctggatac t 21

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 gene-specific RT-PCR amplification forward primer

<400> 7
cgaaagcttc agagatgtct tcca 24

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 gene-specific RT-PCR amplification reverse primer

<400> 8
aatggatccc tttgaacagt attccac 27

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 RT-PCR product forward primer for cloning into pET28a vector

<400> 9
atagaattca tgtcttccag aagtac 26

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 RT-PCR product reverse primer for cloning into pET28a vector

<400> 10
tatctcgagc tttgaacagt at 22

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> H1RNA gene containing promoter region genomic fragment PCR amplification primer for siRNA plasmid vector

<400> 11
tggtagccaa gtgcaggtta ta 22

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> H1RNA gene containing promoter region genomic fragment PCR amplification primer for siRNA plasmid vector

<400> 12
ccaaagggtt tctgcagttt ca 22

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> BamHI and XhoI fragment containing H1RNA PCR amplification primer

<400> 13
tgcggatcca gagcagattg tactgagagt 30

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> BamHI and XhoI fragment containing H1RNA PCR amplification primer

<400> 14
ctctatctcg agtgaggcgg aaagaacca 29

<210> 15
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR amplification primer for ligated DNA template

<400> 15
tttaagcttg aagaccattt ttggaaaaaa aaaaaaaaaa aaaaaac 47

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR amplification primer for ligated DNA template

<400> 16
tttaagcttg aagacatggg aaagagtggt ctca 34

<210> 17
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> double-stranded oligonucleotide for cloning control plasmid psiH1BX-EGFP

<400> 17
caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c 51

<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> double-stranded oligonucleotide for cloning
control plasmid psiH1BX-EGFP

<400> 18
aaaagaagca gcacgacttc ttctctcttg aagaagaagt cgtgctgctt c 51

<210> 19
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> double-stranded oligonucleotide for cloning into
psiH1BX3.0 vector plasmid expressing C10orf3-siRNA
(psiH1BX-C10orf3-G)

<400> 19
tcccggagag actgaaaaca gagttcaaga gactctgttt tcagtctctc c 51

<210> 20
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> double-stranded oligonucleotide for cloning into
psiH1BX3.0 vector plasmid expressing C10orf3-siRNA
(psiH1BX-C10orf3-G)

<400> 20
aaaaggagag actgaaaaca gagtctcttg aactctgttt tcagtctctc c 51

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 siRNA oligonucleotide target sequence

<400> 21
ggagagactg aaaacagag 19

<210> 22
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 siRNA oligonucleotide hairpin loop structure

<400> 22
ggagagactg aaaacagagt tcaagagact ctgttttcag tctctcc 47

<210> 23
<211> 488
<212> DNA
<213> Artificial

<220>
<223> psiH1 BX3.0 vector plasmid sequence upstream of siRNA
DNA fragment insertion site

<400> 23
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctggat 60
ccactagtaa cggccgccag tgtgctggaa ttcggcttgg tagccaagtg caggttatag 120
ggagctgaag ggaaaggggt cacagtaggt ggcatcgttc ctttctgact gcccgccccc 180
cgcatgccgt cccgcgatat tgagctccga acctctcgcc ctgccgccgc cggtgctccg 240
tcgccgccgc gccgccatgg aattcgaacg ctgacgtcat caacccgctc caaggaatcg 300
cgggcccagt gtcactaggc gggaacaccc agcgcgcgtg cgccctggca ggaagatggc 360
tgtgagggac aggggagtgg cgccctgcaa tatttgcatg tcgctatgtg ttctgggaaa 420
tcaccataaa cgtgaaatgt ctttggattt gggaatctta taagttctgt atgagaccac 480
tctttccc 488

<210> 24
<211> 4597
<212> DNA
<213> Artificial

<220>
<223> psiH1 BX3.0 vector plasmid sequence downstream of siRNA
DNA fragment insertion site

<400> 24
tttttgggaa aaaaaaaaaa aaaaaaaaaa cgaaaccggg ccgggcgcgg tggttcacgc 60
ctataatccc agcactttgg gaggccgagg cgggcggatc acaaggtcag gaggtcgaga 120
ccatccaggc taacacggtg aaacccccccc ccatctctac taaaaaaaaa aaatacaaaa 180
aattagccat tagccgggcg tggtggcggg cgcctataat cccagctact tgggaggctg 240
aagcagaatg gcgtgaaccc gggaggcgga cgttgcagtg agccgagatc gcgccgactg 300
cattccagcc tgggcgacag agcgagtctc aaaaaaaaaa ccgagtggaa tgtgaaaagc 360
tccgtgaaac tgcagaaacc caagccgaat tctgcagata tccatcacac tggcggccgc 420
tcgagtgagg cggaaagaac cagctggggc tctaggggggt atccccacgc gccctgtagc 480
ggcgcattaa gcgcggcggg tgtggtggtt acgcgcagcg tgaccgctac acttgccagc 540
gccctagcgc ccgctccttt cgctttcttc ccttcctttc tcgccacgtt cgccggcttt 600
ccccgtcaag ctctaaatcg ggggctccct ttagggttcc gatttagtgc tttacggcac 660
ctcgacccca aaaaacttga ttagggtgat ggttcacgta gtgggccatc gccctgatag 720
acggtttttc gccctttgac gttggagtcc acgttcttta atagtggact cttgttccaa 780
actggaacaa cactcaaccc tatctcggtc tattcttttg atttataagg gattttgccg 840
atttcggcct attggttaaa aaatgagctg atttaacaaa aatttaacgc gaattaattc 900
tgtggaatgt gtgtcagtta gggtgtggaa agtccccagg ctccccagca ggcagaagta 960
tgcaaagcat gcatctcaat tagtcagcaa ccaggtgtgg aaagtcccca ggctccccag 1020
caggcagaag tatgcaaagc atgcatctca attagtcagc aaccatagtc ccgcccctaa 1080
ctccgcccat cccgcccctа actccgccca gttccgccca ttctccgccc catggctgac 1140
taatttttt tatttatgca gaggccgagg ccgcctctgc ctctgagcta ttccagaagt 1200
agtgaggagg ctttttttgga ggcctaggct tttgcaaaaa gctcccggga gcttgtatat 1260
ccattttcgg atctgatcaa gagacaggat gaggatcgtt tcgcatgatt gaacaagatg 1320
gattgcacgc aggttctccg gccgcttggg tggagaggct attcggctat gactgggcac 1380
aacagacaat cggctgctct gatgccgccg tgttccggct gtcagcgcag gggcgcccgg 1440
ttctttttgt caagaccgac ctgtccggtg ccctgaatga actgcaggac gaggcagcgc 1500
ggctatcgtg gctggccacg acgggcgttc cttgcgcagc tgtgctcgac gttgtcactg 1560
aagcgggaag ggactggctg ctattgggcg aagtgccggg gcaggatctc ctgtcatctc 1620
accttgctcc tgccgagaaa gtatccatca tggctgatgc aatgcggcgg ctgcatacgc 1680
ttgatccggc tacctgccca ttcgaccacc aagcgaaaca tcgcatcgag cgagcacgta 1740
ctcggatgga agccggtctt gtcgatcagg atgatctgga cgaagagcat caggggctcg 1800
cgccagccga actgttcgcc aggctcaagg cgcgcatgcc cgacggcgag gatctcgtcg 1860

tgacccatgg cgatgcctgc ttgccgaata tcatggtgga aaatggccgc ttttctggat 1920
tcatcgactg tggccggctg ggtgtggcgg accgctatca ggacatagcg ttggctaccc 1980
gtgatattgc tgaagagctt ggcggcgaat gggctgaccg cttcctcgtg ctttacggta 2040
tcgccgctcc cgattcgcag cgcatcgcct tctatcgcct tcttgacgag ttcttctgag 2100
cgggactctg gggttcgaaa tgaccgacca agcgacgccc aacctgccat cacgagattt 2160
cgattccacc gccgccttct atgaaaggtt gggcttcgga atcgttttcc gggacgccgg 2220
ctggatgatc ctccagcgcg gggatctcat gctggagttc ttcgcccacc ccaacttgtt 2280
tattgcagct tataatggtt acaaataaag caatagcatc acaaatttca caaataaagc 2340
attttttca ctgcattcta gttgtggttt gtccaaactc atcaatgtat cttatcatgt 2400
ctgtataccg tcgacctcta gctagagctt ggcgtaatca tggtcatagc tgtttcctgt 2460
gtgaaattgt tatccgctca caattccaca caacatacga gccggaagca taaagtgtaa 2520
agcctggggt gcctaatgag tgagctaact cacattaatt gcgttgcgct cactgcccgc 2580
tttccagtcg ggaaacctgt cgtgccagct gcattaatga atcggccaac gcgcggggag 2640
aggcggtttg cgtattgggc gctcttccgc ttcctcgctc actgactcgc tgcgctcggt 2700
cgttcggctg cggcgagcgg tatcagctca ctcaaaggcg gtaatacggt tatccacaga 2760
atcaggggat aacgcaggaa agaacatgtg agcaaaaggc cagcaaaagg ccaggaaccg 2820
taaaaaggcc gcgttgctgg cgtttttcca taggctccgc ccccctgacg agcatcacaa 2880
aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga ctataaagat accaggcgtt 2940
tccccctgga agctccctcg tgcgctctcc tgttccgacc ctgccgctta ccggatacct 3000
gtccgccttt ctcccttcgg gaagcgtggc gctttctcat agctcacgct gtaggtatct 3060
cagttcggtg taggtcgttc gctccaagct gggctgtgtg cacgaacccc ccgttcagcc 3120
cgaccgctgc gccttatccg gtaactatcg tcttgagtcc aacccggtaa gacacgactt 3180
atcgccactg gcagcagcca ctggtaacag gattagcaga gcgaggtatg taggcggtgc 3240
tacagagttc ttgaagtggt ggcctaacta cggctacact agaagaacag tatttggtat 3300
ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt ggtagctctt gatccggcaa 3360
acaaaccacc gctggtagcg gtttttttgt ttgcaagcag cagattacgc gcagaaaaaa 3420
aggatctcaa gaagatcctt tgatcttttc tacggggtct gacgctcagt ggaacgaaaa 3480
ctcacgttaa gggattttgg tcatgagatt atcaaaaagg atcttcacct agatcctttt 3540
aaattaaaaa tgaagtttta aatcaatcta aagtatatat gagtaaactt ggtctgacag 3600
ttaccaatgc ttaatcagtg aggcacctat ctcagcgatc tgtctatttc gttcatccat 3660
agttgcctga ctccccgtcg tgtagataac tacgatacgg gagggcttac catctggccc 3720
cagtgctgca atgataccgc gagacccacg ctcaccggct ccagatttat cagcaataaa 3780
ccagccagcc ggaagggccg agcgcagaag tggtcctgca actttatccg cctccatcca 3840
gtctattaat tgttgccggg aagctagagt aagtagttcg ccagttaata gtttgcgcaa 3900
cgttgttgcc attgctacag gcatcgtggt gtcacgctcg tcgtttggta tggcttcatt 3960
cagctccggt tcccaacgat caaggcgagt tacatgatcc cccatgttgt gcaaaaaagc 4020
ggttagctcc ttcggtcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact 4080
catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgcttttc 4140
tgtgactggt gagtactcaa ccaagtcatt ctgagaatag tgtatgcggc gaccgagttg 4200
ctcttgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtgct 4260
catcattgga aaacgttctt cggggcgaaa actctcaagg atcttaccgc tgttgagatc 4320
cagttcgatg taacccactc gtgcacccaa ctgatcttca gcatctttta ctttcaccag 4380
cgtttctggg tgagcaaaaa caggaaggca aaatgccgca aaaaagggaa taagggcgac 4440
acggaaatgt tgaatactca tactcttcct ttttcaatat tattgaagca tttatcaggg 4500
ttattgtctc atgagcggat acatatttga atgtatttag aaaaataaac aaatagggggt 4560
tccgcgcaca tttccccgaa aagtgccacc tgacgtc 4597

<210> 25
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> 2-10 u nucleotides added to 3' end of antisense strand of target sequence to enhance siRNA inhibition activity

<221> modified_base
<222> (3)...(10)
<223> u or absent

<400> 25
uuuuuuuuuu 10

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> poly dT-12-18 primer

<221> modified_base
<222> (13)...(18)
<223> t or absent

<400> 26
tttttttttt tttttttt 10